

GATGGGAACACGACA [REDACTED] TCATTGTCCACTATTTGCCCT [REDACTED] GTGATTATCACCTGGAGTCTAT

70

Asp Gly Asn Thr Thr Ile Ile Val His Tyr Phe Cys Pro Ala Gly Asp Tyr Gln Pro Trp Ser Leu

GGATGTGGCCAAAAGACGGAGGTGGGCTGAATACGATTCAATCAACCGGCTGACTCTTTGGAGCTGT

140

Trp Met Trp Pro Lys Asp Gly Gly Ala Glu Tyr Asp Phe Asn Gln Pro Ala Asp Ser Phe Gly Ala Val

TGCAAGTGCTGATATTCAGGAAACCCAAGTCAGGTAGGAATTATCGTCGCACTCAAGATTGGACCAA

210

Ala Ser Ala Asp Ile Pro Gly Asn Pro Ser Gln Val Gly Ile Ile Val Arg Thr Gln Asp Trp Thr Lys

GATGTGAGCGCTGACCGCTACATAGATTAAAGCAAAGGAAATGAGGTGTGGCTTGTAGAAGGAAACAGCC

280

Asp Val Ser Ala Asp Arg Tyr Ile Asp Leu Ser Lys Gly Asn Glu Val Trp Leu Val Glu Gly Asn Ser

AAATTTTTATAATGAAAAAGATGCTGAGGATGCAGCTAACCCGCTGTAAGCAACGCTTATTAGATGC

350

98

102

Gln Ile Phe Tyr Asn Glu Lys Asp Ala Glu Asp Ala Ala Lys Pro Ala Val Ser Asn Ala Tyr Leu Asp Ala

TTCAAACCAGGTGCTGGTTAAACTTAGCCAGCCGTTAACCTTGGGGAGGNNAAGCGGCTTACGGTT

420

Ser Asn Gln Val Leu Val Lys Leu Ser Gln Pro Leu Thr Leu Gly Glu Gly ??? Ser Gly Phe Thr Val

CATGACGACACAGCAAATAAGGATATTCCAGTGACATCTGTGAAGGATGCAAGTCTGGTCAAGATGTAA

490

His Asp Asp Thr Ala Asn Lys Asp Ile Pro Val Thr Ser Val Lys Asp Ala Ser Leu Gly Gln Asp Val

CCGCTGTTGGCAGGTACCTCCAACATATTTGGAGGTTCCGATTGGGCACCTGATAATCACAGTAC

560

Thr Ala Val Leu Ala Gly Thr Phe Gln His Ile Phe Gly Gly Ser Asp Trp Ala Pro Asp Asn His Ser Thr

FIGURE 1A

TTTATTAAAAAGGTGAAACAATCTCTATCAATTCTCAGGA

630

Leu Leu Lys Lys Val Thr Asn Asn Leu Tyr Gln Phe Ser Gly Asp Leu Pro Glu Gly Asn Tyr Gln Tyr

AAAGTGGCTTAAATGATAGCTGGAATAATCCGAGTTACCCATCTGACAACATTAATTAACAGTCCCTG

700

Lys Val Ala Leu Asn Asp Ser Trp Asn Asn Pro Ser Tyr Pro Ser Asp Asn Ile Asn Leu Thr Val Pro

CCGGCGGTGCACACGTCACTTTCTGATATTCCGTCCACTCATGCAGTCTATGACACAATTAAATAATCC

770

Ala Gly Gly Ala His Val Thr Phe Ser Tyr Ile Pro Ser Thr His Ala Val Tyr Asp Thr Ile Asn Asn Pro

TAATGCGGATTACAAGTAGAAAGCGGGGTTAAACGGATCTCGTACGGTTACTCTAGGGAAAGATCCA

840

Asn Ala Asp Leu Gln Val Glu Ser Gly Val Lys Thr Asp Leu Val Thr Val Thr Leu Gly Glu Asp Pro

GATGTGAGCCATACTCTGCCATTCAAACAGATGGCTATCAGGCAAAGCAGGTGATACTCGTAATGTGC

910

Asp Val Ser His Thr Leu Ser Ile Gln Thr Asp Gly Tyr Gln Ala Lys Gln Val Ile Pro Arg Asn Val

TAAATTCCATCACAGTACTACTATTAGGAGATGATCTGGGAATACCTATACACAGAAAGCAACACCTT

980

Leu Asn Ser Ser Gln Tyr Tyr Ser Gly Asp Asp Leu Gly Asn Thr Tyr Thr Gln Lys Ala Thr Thr Phe

309 Y

TAAAGTCTGGCACCAACTCTACTCAAGTAAATGTTCTTATGACAGTGCAACGGTTCTGTAACA

1050

VWAP

Lys Val Trp Ala Pro Thr Ser Thr Gln Val Asn Val Leu Leu Tyr Asp Ser Ala Thr Gly Ser Val Thr

AAAATCGTACCTATGACGGCATGGGCATGGTGTGGAGCAACGGTTAATCAAAACCTTGAAAATT

1120

Lys Ile Val Pro Met Thr Ala Ser Gly His Gly Val Trp Glu Ala Thr Val Asn Gln Asn Leu Glu Asn

FIGURE 1B

GGTATTACATGTATGAAACAGGCCAAGGCTCTACCCGAACCTGTTGATCCTATGCAACTGCGAT

1180

391 DPY

Trp Tyr Tyr Met Tyr Glu Val Thr Gly Gln Gly Ser Thr Arg Thr Ala Val Asp Pro Tyr Ala Thr Ala Ile

TGCACCAAATGGAACGAGAGGCATGATTGTGGACCTGGCTAAAACAGATCCTGCTGGCTGGAACAGTGAT

1260

Ala Pro Asn Gly Thr Arg Gly Met Ile Val Asp Leu Ala Lys Thr Asp Pro Ala Gly Trp Asn Ser Asp

AAACATATTACGCCAAAGAACATAGAACATGAGGTACATCTATGAAATGGATGTCCGTACTTTCCATTG

1330

433

A

Lys His Ile Thr Pro Lys Asn Ile Glu Asp Glu Val Ile Tyr Glu Met Asp Val Arg Asp Phe Ser Ile

ACCCTAATTGGGTATGAAAAATAAGGGAAAGTATTGGCTTACAGAAAAGGAACAAAGGGCCCTGA

1400

B

Asp Pro Asn Ser Gly Met Lys Asn Lys Gly Lys Tyr Leu Ala Leu Thr Glu Lys Gly Thr Lys Gly Pro Asp.

CAACGTAAAGACGGGGATAGATTCTTAAACAACTGGGATTACTCATGTTAGCTTATGCCTGTTTC

1470

C

Asn Val Lys Thr Gly Ile Asp Ser Leu Lys Gln Leu Ile Thr His Val. Gln Leu Met Pro Val Phe

GCATCTAACAGTGTGATGAAACTGATCCAACCCAAAGATAATTGGGTTATGACCCCTGCAACTATGATG

1540

YNWGY

Ala Ser Asn Ser Val Asp Glu Thr Asp Pro Thr Gln Asp Asn Trp Gly Tyr Asp Pro Arg Asn Tyr Asp

TTCCTGAAGGGCAGTATGCTACAAATGCGAATGTAATGCTCGTATAAAGAGTTAAGGAAATGGTTCT

1610

Val Pro Glu Gly Gln Tyr Ala Thr Asn Ala Asn Gly Asn Ala Arg Ile Lys. Glu Phe Lys Glu Met Val Leu

TTCACTCCATCGTAACACATTGGGTTAACATGGATGTTGTCTATAATCACCTTGCCACGCAAATC

1640

541

I

Ser Leu His Arg Glu His Ile Gly Val Asn Met Asp Val Val Tyr Asn His Thr Phe Ala Thr Gln Ile

FIGURE 1C

TCTGACTTCGATAAA GTACCAGAATATTATTACCGTACGA GATCCAGGTAATTATACCAACGGATC

D

1750

Ser Asp Phe Asp Lys Ile Val Pro Glu Tyr Tyr Arg Thr Met Ile Gln Val Ile Ile Pro Thr Asp

AGGTACTGGAAATGAAATTGCANGCNGAAAGGCCAATGGTTCAAAAATTATTATTGATTCCCTTAAGTA

1820

Gln Val Leu Glu Met Lys Leu ??? Ala Glu Arg Pro Met Val Gln Lys Phe Ile Ile Asp Ser Leu Lys Tyr

TTGGGTCAATGAGTATCATATTGACGGCTTCCGTTTGACTTAATGGCGCTGCTGGAAAAGACACGATG

1890

II

Trp Val Asn Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Leu Met Ala Leu Leu Gly Lys Asp Thr Met

TCCAAAGCTGCCTCGGAGCTTCATGCTATTAATCCAGGAATTGCACTTACGGTGAGCCATGGACGGGTG

1960

D

III

Ser Lys Ala Ala Ser Glu Leu His Ala Ile Asn Pro Gly Ile Ala Leu Tyr Gly Glu Pro Trp Thr Gly

D

GAACCTCTGCACTGCCAGATGATCAGCTTCTGACAAAAGGAGCTAAAAAGGCATGGAGTAGCGGTGTT

2030

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TAATGATTCCGAAGCGGATCGGATTAAATGGATGAACTCGCACAGCAGTTGTTATGACCTCACAGGC

2310

Asn Asp Ser Glu Ala Asp Arg Ile Lys Met Asp Glu Leu Ala Gln Ala Val Val Met Thr Ser Gln Gly

E

GTTCCATTGCAAGGCAGGGAGAAATGCTTCGTANAAAAGGCGGCAACGACAATAGTTATAATGCAG

2380

Val Pro Phe Met Gln Gly Gly Glu Glu Met Leu Arg ??? Lys Gly Gly Asn Asp Asn Ser Tyr Asn Ala

GCGATGCGGTCAATGAGTTGATTGGAGCAGGAAAGCTCAATATCCAGATGTTTCAACTATTATAGCGG

2450

Gly Asp Ala Val Asn Glu Phe Asp Trp Ser Arg Lys Ala Gln Tyr Pro Asp Val Phe Asn Tyr Tyr Ser Gly

GCTAACCTTCGTCTTGATCACCCAGCCTTCCGCATGACGACAGCTAATGAAATCAATAGCCACCTC

2520

Leu Ile His Leu Arg Leu Asp His Pro Ala Phe Arg Met Thr Thr Ala Asn Glu Ile Asn Ser His Leu

CAATTCTAAATAGTCCAGAGAACACAGTGGCCTATGAATTAACGTGATCATGTTAATAAGACAAATGGG

2590

Gln Phe Leu Asn Ser Pro Glu Asn Thr Val Ala Tyr Glu Leu Thr Asp His Val Asn Lys Asp Lys Trp

GAAATATCATTGTTTATAACCCAAATAAAACTGTAGCAACCATCAATTGCCGAGCGGGAAATGGGC

2660

Gly Asn Ile Ile Val Val Tyr Asn Pro Asn Lys Thr Val Ala Thr Ile Asn Leu Pro Ser Gly Lys Trp Ala

AATCAATGCTACGAGCGGTAGGTAGGAGAACCTGGTCAAGCAGAGGGAAAGTGTCCAAGTACCA

2730

Ile Asn Ala Thr Ser Gly Lys Val Gly Glu Ser Thr Leu Gly Gln Ala Glu Gly Ser Val Gln Val Pro

GGTATATCTATGATGATCCTTCATCAAGAGGTAGGCCAGACCACGGTAAAAAGTAATAGAAAAA

2794

Gly Ile Ser Met Met Ile Leu His Gln Glu Val Ser Pro Asp His Gly Lys Lys

FIGURE 1E

FIGURE 2A

XXXXIQTA ~~XX~~ ----- VLXXXXYY ~~GEXL~~ -- GAXYT Majority

330

340

Y

350

360

313 HTLSIQTDGYQAKQVIPRNVLNSSQYYSGDDL--GNTYT pullseqsig.seq.PRO  
281 SATQVQTAG-----VLDDA-YAEAAEALSYSYGAQLA klebpnseqsig.seq.p  
91 ---IRTAAFDD-----EFYYDGE-L--GAVYT subpull.seq.pro

XXXTTFKVWAPTA T Q V X V X L Y X X X X X X X X X M T X S X X G Majority

VWAP 370

380

390

400

351 QKATTTFKVWAPTS T Q V N V L L Y D S A T G S V T K I V P M T A S G H G pullseqsig.seq.PRO  
310 DGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRDSASG klebpnseqsig.seq.p  
112 ADHTVFKVWAPAA T S A A V K L S H P N K S G -- R T F Q M T R L E K G subpull.seq.pro

VWXXTVXXDLXGXXYYXXTX - XXXXR ----- EXVDPYAX Majority

410

420

430

D PY 440

391 VWEATVNQNLLENWYYMYEVTG-QGSTR---TAVDPYAT pullseqsig.seq.PRO  
350 AWSWQGGSDLKGAFYRYAMTVYHPQSRSRKVEQYEVTDPYAH klebpnseqsig.seq.p  
150 VYAVTVTGTGDLLHGYEYLFCICN-NSEWM---ETVDQYAK subpull.seq.pro

AXXXNGEXGXVVDLXXXD -- P X G W X X X X P X X X X X D X V - Majority

450

460

470

480

425 AIAPNGTRGMIVDLAKTD--PAGWNSDKHITPKNIEDDEV pullseqsig.seq.PRO  
390 SLSTNSEYESQVVVDLNDSALKPDGWDNLTMMPHAQKTKADLA klebpnseqsig.seq.p  
184 AVTVNGEKGVVL---RPD--QMKWTAPLKPFSSH PV-DAV- subpull.seq.pro

---IYEXHXR'DFSI-DXNSGMXNKGYLALT EXDT XXXXX Majority

A

490

B

510

520

462 ---IYEMDVRDFSI-DPNNSGMKNKGKYLALT EKGTKGP DN pullseqsig.seq.PRO  
430 KMTIHESHIRDLSAWDQTVPAAELLRGKYLALT AGDSNMVQH klebpnseqsig.seq.p  
217 ---IYETHLRRDFSI-HENSGMINKGKYLALT ETDTQTANG subpull.seq.pro

XKTGXXXLKLGVTHVELLPVFDXAXVDE----- Majority

530

C

540

550

560

498 VKTGIDSLKQLGITHVQLMPVFASNSVDE----- pullseqsig.seq.PRO  
470 LKT---LSASGVTHVELLPVFDLATVN EFSDKVADIQQP klebpnseqsig.seq.p  
253 SSSGLAYVKELGVTHVELLPVNDFAGVDE----- subpull.seq.pro

-----X Majority

570

580

590

600

527 -----T-----T pullseqsig.seq.PRO  
506 FSRLCEVN SAVKSSEFAGYCD SG STVEEV LNQLKQSDSQD klebpnseqsig.seq.p  
282 -----E-----E subpull.seq.pro

X P -----TDXYNWGYD.PXHYXVPEGSYATNPXGX Majority

610

620

630

640

528 DP-----TQD-NWGYDPRNYDVPEGQYATNANG- pullseqsig.seq.PRO  
546 NPQVQALNTLVAQTD SYNWGYDPPFH YTVPEGSYATDPEGT klebpnseqsig.seq.p  
283 KP-----LDAYNWGYNPLHFFAPEGSYASNPHD P subpull.seq.pro

YNWGY

FIGURE 2B

## FIGURE 2C

D X X N X X D W S R X X X - - - - -					Majority
--	970	980	990	1000	
824	DAVNEFDWSRKAQ				pullseqsig.seq.PF
903	DWFNRVDYSLQDNNYNVGMPRI	SDDGSNYEVITRVKEMVA			klebpnseqsig.seq.
586	DSINQLDWDRRET				subpull.seq.pro
- - - - X K X X X X Y Y X X L I X L R K X H P A F R L X X A X X I X X H L X					Majority
	1010	1020	1030	1040	
837	- - - - Y P D V F N Y Y S G L I H L R L D H P A F R M T T A N E I N S H L Q				pullseqsig.seq.PF
943	T P G E A E L K Q M T A F Y Q E L T E L R K S S P L F T L G D G S A V M K R V D				klebpnseqsig.seq.
599	- - - - F K E D V H Y I R R L I S L R K A H P A F R L R S A A D I Q R H L E				subpull.seq.pro
F L N X X E X - - - - T V A Y X L X D X X X X D X W - X X I I V X X N A					Majority
	1050	1060	1070	1080	
871	F L N S P E N - - - - T V A Y E L T D H V N K D K W - G N I I V V Y N P				pullseqsig.seq.PR
983	F R N T G S D Q Q A G L L V M T V D D G M K A G A S L D S R L D G L V V A I N A				klebpnseqsig.seq.
633	C L T L K E H - - - - L I A Y R L Y D L D E V D E W - K D I I V I H H A				subpull.seq.pro
X P X S X T X N L P X G X X X X L X A X S G X X G E X T L X X - - - A X G					Majority
	1090	1100	1110	1120	
902	N K T V A T I N L P S G K - - W A I N A T S G K V G E S T L G Q - - - A E G				pullseqsig.seq.PR
1023	A P E S R T L N E F A G E T L - Q L S A I Q Q T A G E N S L A N G V Q I A A D G				klebpnseqsig.seq.
664	S P D S V E W R L P N D I P Y R L L C D P S G F Q E D P T - - E - - - I K K				subpull.seq.pro
T V X V P G - - I X X X I L X Q X X A X D X G - X K S X X - -					Majority
	1130	1140	1150		
935	S V Q V P G - - I S M M I L H Q E V S P D H G - K K - - . K				pullseqsig.seq.PR
1062	T V T L P A W S V A V L E L P Q G E A Q G A G L P V S S K				klebpnseqsig.seq.
697	T V A V N G - - I G T V I L Y - - L A S D L - - K S F A				subpull.seq.pro

FIGURE 2D

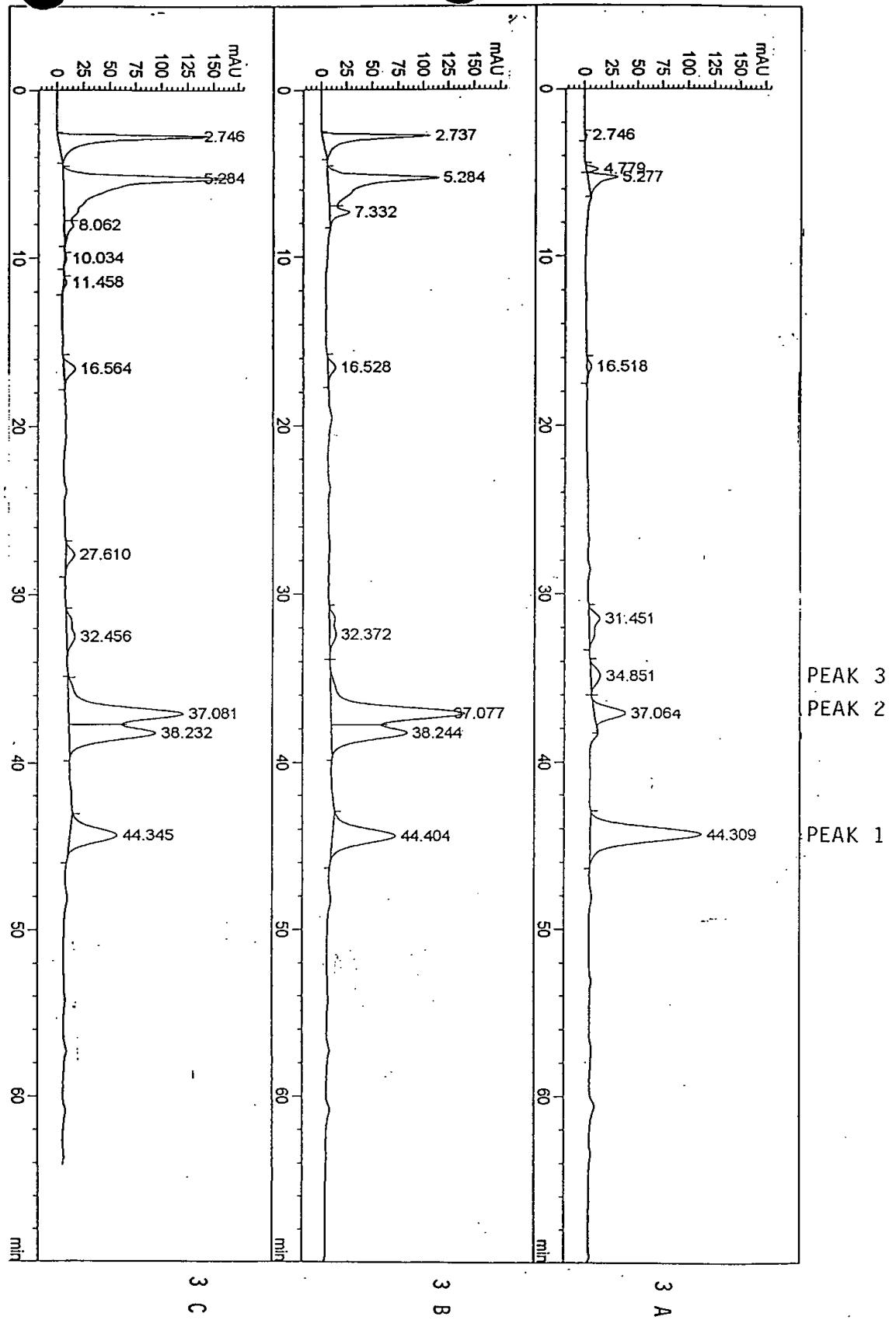
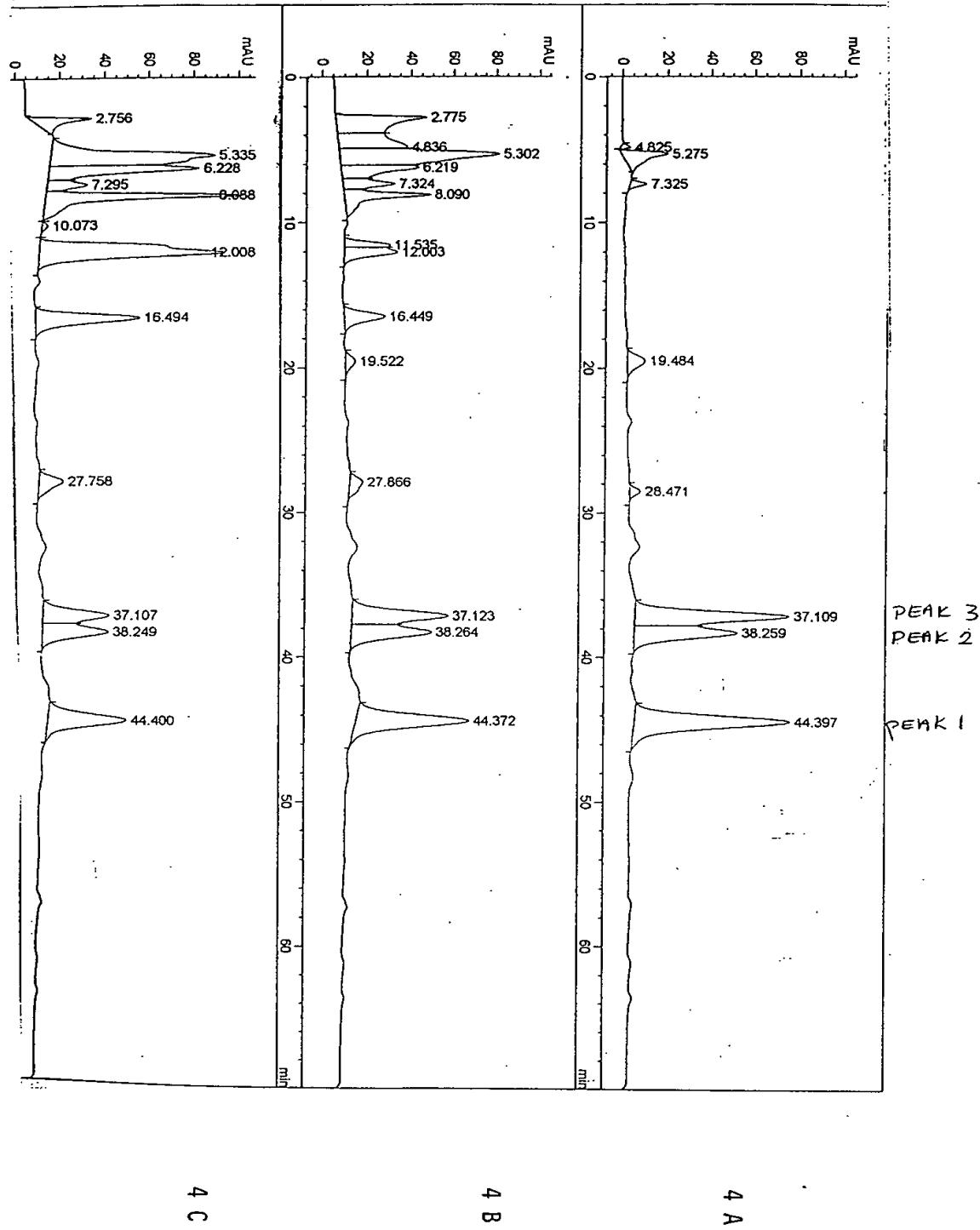


FIGURE 3 A, 3.B, 3 C

FIGURE 4 A, 4 B, 4 C



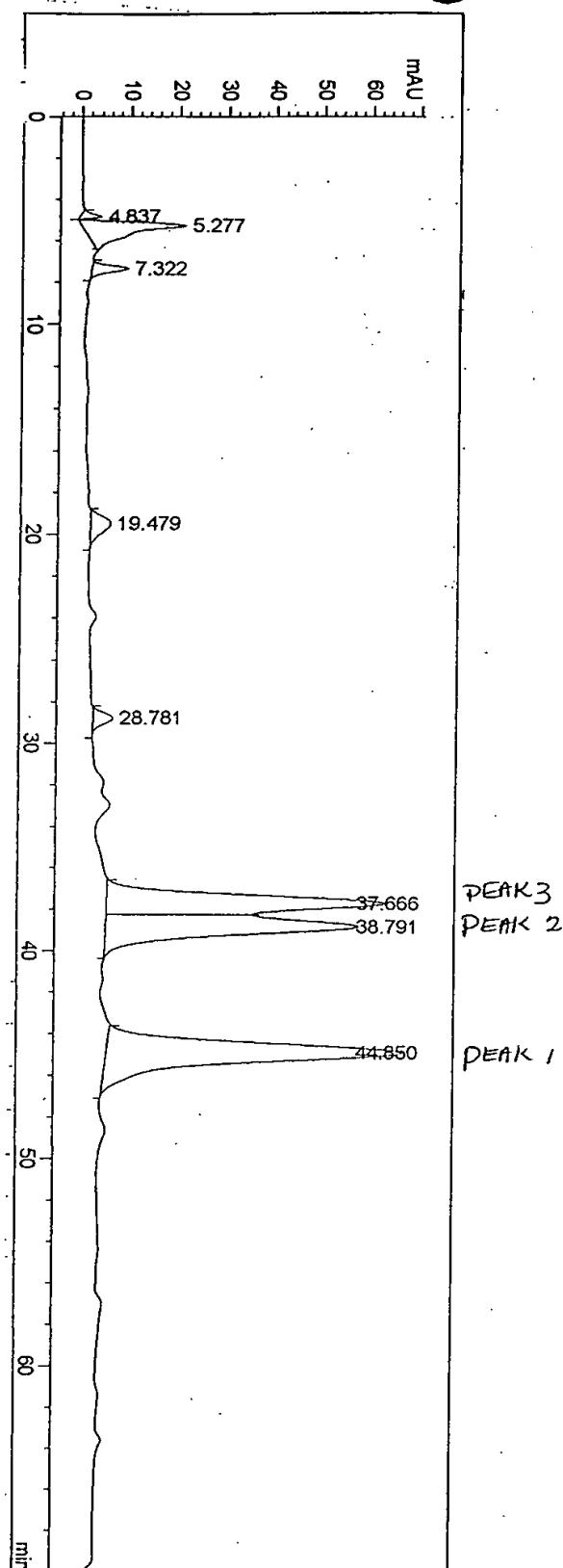


FIGURE 4 D

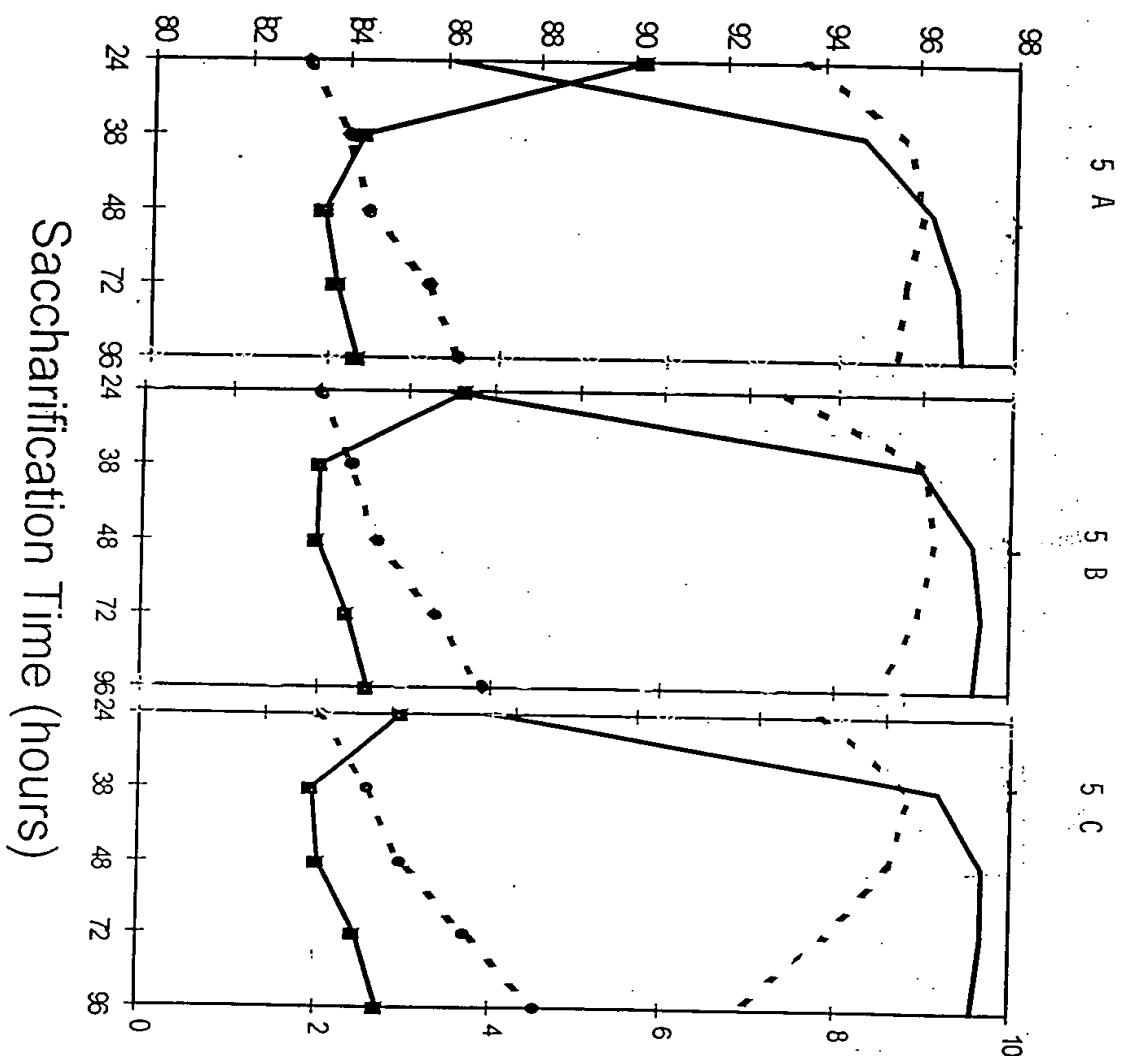


FIGURE 5 A, 5 B, 5 C

## Percent Maximum Glucose Yield

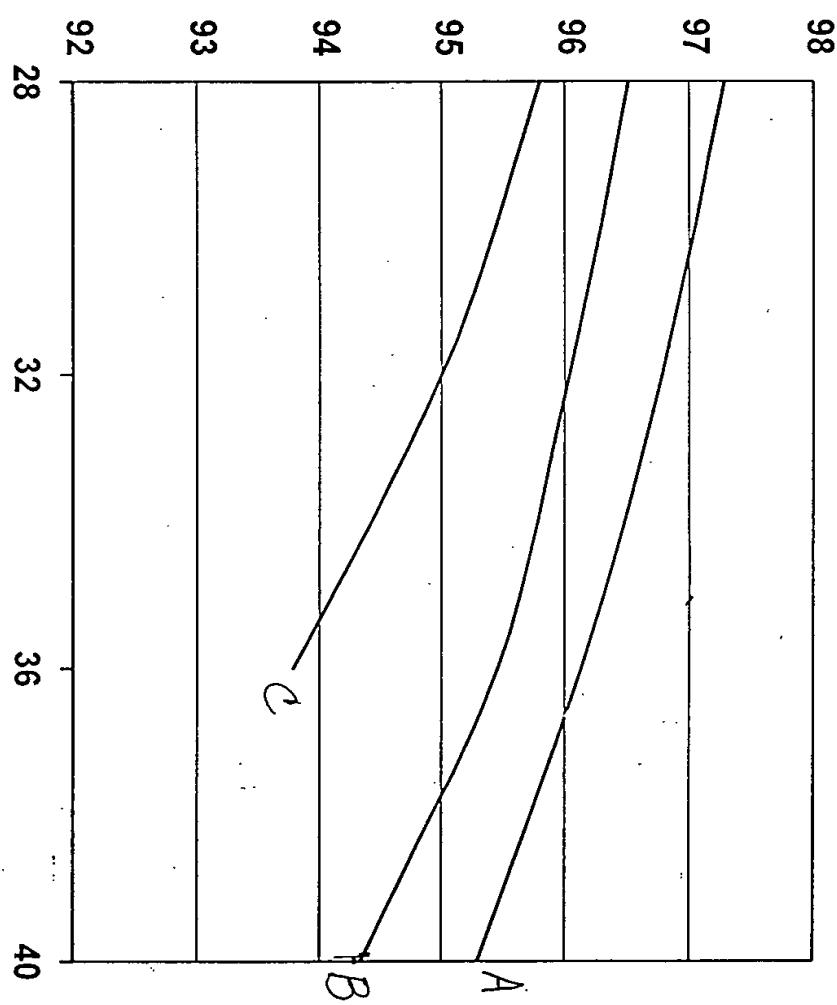


FIGURE 6